128

108





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48

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Like cDNA (SEQ ID NO:1) and Sequences Amino Acid (SEQ ID NO:2) Figure 1 Map of Human IL-17

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₩,	CTCAAGTCACTCCCTAAAAAGACAGTGGAAATAAATTTGAATAAACAAAACAGGCTTGCT
61 121	GAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGTCAG TCAGTGCCCCACTTGTGACTGAGTGTGCAGTGCCCAGCATGTACCAGGTGGTTGCATTCT
	M Y Q V A F L
181	TGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAG
σ	A M V M G T H T Y S H W P S C C P S K G
241	GGCAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGC
29	Q D T S E E L L R W S T V P V P P L E P
301	CTGCTAGGCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACA
49	ARPNRHPESCRASEDGPLNS
361	SCCATO
69	RAISPWRYELDRDLNRLPQD
421	ACCTGTACCACGCCCGTTGCCTGTGCCCGCACTGCGTCAGCCTACAGACAG
8	LYHARCLCPHCVSLQTGSHM
481	TGGACCCCCGGGGCAACTCGGAGCTGCTCTACCACAACCAGACTGTCTTCTACCGGCGGC
109	DPRGNSELLYHNQTVFYRP
541	CATGCCATGGCGAGAAGGGCACCCACAAGGGCTACTGCCTGGAGCGCAGGCTGTACCGTG
129	CHGEKGTHKGYCLERRLYRV
601	TTTCCTTAGCTTGTGTGTGTGCGCCCCGTGTGATGGGCTAG 643
149	SLACVCVRPRVMG*162



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and Amino Acid Peptide Signal ID NO:3) Predicted Figure 2A cDNA (SEQ (Map of Mouse IL-17 Like CDNA Sequences ID NO:4) (SEQ

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⊣	æs	\TG	TAC	SCAC.	SGC	TGT	JGC	ATT	CTI	56	AAT	GAT	CGI	999	AAC	CCA	CAC	CGT	CAG(<u> </u>
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118	9900	3AG	GAG	,TG(3CT)	GAA	GTG	3GAG	CTO	TGC	ATC	TGT	GTC	CCC	CCC	AGA	CCC	TCT	GAG(CCGGAGGAGTGGCTGAGTGGAGCTCTGCATCTGTGTCCCCCCCC
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51	H	h y 1	H	Ø	田	ഗ	ပ	ద	Ø	ß	서	Ω	Ö	Д	口	Z	ഗ	ĸ	Ø	н
238	TCTC	CT	'TGC	;AG(CTA	TGA	GTT	GGA	CAG	3GGZ	\CT1	GAA	TCG	GGT	CCC	CCA	GGA	CCT	GTA(CCAC
71	N H	٠.	×	ß	×	Ы	Ы	Ω	ద	Ω	Ч	Z	卍	>	д	Ø	Ω	ᄓ	×	H
298	GCTC	GA	TGC	CT	3TG	CCC	ACA	CTC	CGJ	CAC	CCT	ACA	GAC	AGG	CTC	CCA	CAT	GGA	CCC	98 GCTCGATGCCTGTGCCCACACTGCGTCAGCCTACAGACAG
91	A F	~	ပ	니	ပ	Д	Ħ	Ö	>	ß	니	Ø	H	ග	ഗ	Ħ	Σ	Ω	Д	u
358	GGCA	AAC	TCC)GT(CCC	ACT	TT	VCC	CAZ	CCZ	AGAC	GGT	CTT	CTA	SCCG	gcg	GCC	ATG	CCA	IGGC
111	Z U	ب	Ŋ	>	Д	Ы	×	Ħ	Z	Ø	H	>	ᅜ	×	ద	ĸ	щ	ပ	H	ტ
418	GAGG	3AA	GGJ	ACC	CCA	TCG	SCCG	CTZ	CTO	CTJ	rggz	\GCG	CAG	GCT	CTA	SCG	AGT	CTC	CTT(BGCT
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160	ر م	1	ပ	>	召	д	ద	>	Z	Ø	*									
538	TGCC	SCG	GTJ	igg(3AG	AGA	GGG	CCZ	rgg1	ZTD:	ACA2	ATCA	CCT	TGC	CAA	TGC	GGG	SSS	GGT	ICAA
598	CCC	CTC	CAZ	AGG	CCC	TAC	CTC	BAAG	CAC	3CAC	3601	ວນນ	999	ACA	AGA	TGG	AGG	ACT	TGG	GGAG
658	AAAC	CTC	TGZ	\CT'.	$\Gamma T T$	GCA	CTJ	rTT!	GG7	AGG	CACT	TTT	999	AAG	GAG	CAG	GTT	SCG	CTT.	AAACTCTGACTTTTGCACTTTTTGGAAGCACTTTTTGGGAAGGAGCAGGTTCCGCTTGTGC



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3/28 Figure 2B

CTGGAAGCCATACTCCTGGCTCCTTTCCCCTGAATCCCCCAACTCCTGGCACAGGCACTT AGCCAGGTGTAATTGCCTTGAAGGATGGTTCTGAGGTGAAAGCTGTTATCGAAAGTGAAG TGCTAGAGGATGCTGTTGTGGCATTTCTACTCAGGAACGGACTCCAAAGGCCTGCTGAC 778 838 898 958

and of Non-Secreted Form of Mouse IL-17 Like cDNA (SEQ ID NO:9), Corresponding Amino Acid Sequence (SEQ ID NO:10 Map

GCACTGGCCAAGGCTGTTGCATTCTTGGCAATGATCGTGGGAACCCACACCGTCAGCTTG CCGGGCCAGGTGCCCTCGGCGCGTCCCAAAGCTTAGGGAAGCTCCAGGTGTCTTGGGAAAT GCCTAGGGTCGAGGGCCATTATCACCTACAAATCAGAATGTGGGAGTGCTATTCTAGAGG TCTCCATCTTTGCCATTGCTGGGTCGCTCAGAAAGTGTGATGGGGGTTGTCCCATTGCCA TTCCAGCCCCGGTTGGCTGCCAGAGGCTTCCTCTGGCGTTGGGTACAGAGGCAGAGAAAG <u> AAACCCCAAATGTCTCCTATGAAAAACAATGTCCCCGTCATCCAGGCCAGATCATTCTGC</u> AGTGTCAACAGTTGAGACAAGAAGCTGGGGTCATTTTCTGTGCCTAAGAGTGCCTGTTCT 121 61 181 241 301 361 421 481

CGGATCCAGGAGGGCTGCAGTCACTTGCCCAGCTGCTGCCCCAGCAAAGAGGAAGAACCC 闰 MIVGTHTV Д ß ტ

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Figure 2C

	20		70		90		110		130		150		161								
CCGGAGGAGTGGCTG	. PEEWLKWSSASVSPPEPLSH	. ACCCACCACGCAGAATCCTGCAGGGCCAGCAAGGATGGCCCCCTCAACAGCAGGGCCATC	THHAESCRASKDGPLNSRAI	TCTCCTTGGAGCTATGAGTTGGACAGGGACTTGAATCGGGTCCCCCAGGACCTGTACCAC		. GCTCGATGCCTGTGCCCACACTGCGTCAGCCTACAGACAG				GAG		TGTGTGTGTGTGCGGCCCCGGGTCATGCTTAGTCATGCTCACCACCTGCCTG	. C V C V R P R V M A *	TGCCCGGTTGGGAGAGGGCCAGGTGTACAATCACCTTGCCAATGCGGGCCGGGTTCAA	. GCCCTCCAAAGCCCTACCTGAAGCAGCAGGCTCCCGGGACAAGATGGAGGACTTGGGGAG	- AAACTCTGACTTTTGCACTTTTTGGAAGCACTTTTGGGAAGGAGCAGGTTCCGCTTGTGC	TGCTAGAGGATGCTGTTGTGGCATTTCTACTCAGGAACGGACTCCAAAGGCCTGCTGACC	. CTGGAAGCCATACTCCTGGCTCCTTTCCCCTGAATCCCCCAACTCCTGGCACAGGCACTT	TCTCCACCTCTCCCCCTTTGCCTTTTGTGTGTTTGTGTGCATGCCAACTCTGCGTGC	AGCCAGGTGTAATTGCCTTGAAGGATGGTTCTGAGGTGAAAGCTGTTATCGAAAGTGAAG	L AGATTTATCCAAATAAACATCTGTGTTTAAAAAAAAAAA
601	31	661	51	721	71	781	91	841	111	901	131	961	151	1021	1081	14	1201	26	1321	38	144



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Figure 3A

hIL-17L (SEQ ID NO:2) hIL-1 Sequence, Family Member Amino Acid Sequence, Pile-Up of Human IL-17 Like Amino Acid Known Human ಥ with

(SEQ ID NO:5)

25.0% identity in 160 AA overlap 155; Smith-Waterman score:

60 SPSKGQ ::	120 RLPQDL :: RYPSVI
50 CHTYSHWPSCC : : SITIPRNPGCI 30	100 110 120 LNSRAISPWRYELDRDLNRLPQDL : : : :: : : : : : : : : : : : \
40 50 60 SMYQVVAFLAMVMGTHTYSHWPSCCPSKGQ : ::: : : : : :: SLLLLLSLEAIVKAGITIPRNPGCPNSEDK 0 30	100 GPLNSRAISPV : : YYNRSTSPV
10 20 30 40 50 60 APVSLLPRGLSVSAPLVTECAVPSMYQVVAFLAMVMGTHTYSHWPSCCPSKGQ : ::: : : : : : : : : 1: :	70 80 100 110 120 DTSEELLRWSTVPVPPLEPARPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDL : :: :: :: : : : : : : : :
20 RGLSVSAPLV MTF	80 7PPLEPARPNR : HNRNTNT
10 XPAPVSLLF	70 LLRWSTVPV :: :: VMVNLNI
XNQDSXP	DTSEELL : :: NFPRTVM 40
hIL-17L hIL-17	hIL-17L hIL-17

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Figure 3B

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VGCTCVTPIVHHVA LACVCVRPRVMA 130 190

150

••

hIL-17L

hIL-17



(SEQ ID NO:2) (SEQ ID NO:6 hIL-17L, Sequence, Sequence, IL-20 Amino Acid Pile-Up of Human IL-17 like Amino Acid Figure a Known Human with

36.7% identity in 90 aa overlap Opt: 175 Initn: 124 175; Smith-Waterman score: Init1: 124 SCORES

RNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLC RWSTVPVPPLEPARPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCL 120 •• 110 <u>-</u> :: -: 100 100 90 80 hIL-17L hIL-20

RPRVMA 190 hIL-17L

ш

hIL-20

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Pile-Up of Human IL-17 Like Amino Acid Sequence, hIL-17L, (SEQ ID NO:2) hIL-17b (SEQ ID NO:7) a Known Human IL-17 Amino Acid Sequence, Family Member Figure with

aa overlap 124 Opt: 178 35.6% identity in 90 Initn: 178; Smith-Waterman score: Init1: 124 SCORES

70 80 90 100 110 120 RWSTVPVPPLEPARPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLC :: ::: :: : ::	RNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLC 70 80 90 120	130
70 RWSTVPVPPLEPARPN	RNIEEMVAQLRNSSEI 70	130 140 PHCVSLQTGSHMDPLC : :: LGCVNPFTMQE-DRSN 130
hIL-17L	hIL-17b	hIL-17L hIL-17b

RPRVMA 190 F 180 hIL-17b hIL-17L

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6A Figure

(SEQ ID NO:2) Member Family hIL-17L Sequence, Known Human NO:8 П IL-17 Like Amino Acid SEQ of Sequence Acid Pile-Up of Human Amino with

Opt: 236 194 Initn: Init1: 149 SCORES aa overlap identity in 171 34.5% 243; Smith-Waterman score:

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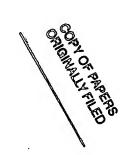


Figure 6

	12 0	130	140	150	160	169
hIL-17L	LNRLPQDLY	HARCLCPHCV	SLQTGSHMDPLO	NSVPLYHNQT	INRLPQDLYHARCLCPHCVSLQTGSHMDPLGNSVPLYHNQTVFYRRPCHGEEGTHR	3THR
hIL-17c	: EDRYPQKLA	: FAECLCRGCI	: : : DARTGRETAAL-	:: -NSVRLLQSLL	: : ::	 SGLPTPG
	120	130	140	150	160	170
	170	180	190			
hIL-17L	RYCLERRLY	RYCLERRLYRVSLACVCVRPRVMA	PRVMA			
	••					
hIL-17c	AFAFHTEFI	AFAFHTEFIHVPVGCTCVLPRSV	PRSV			
	180	190				

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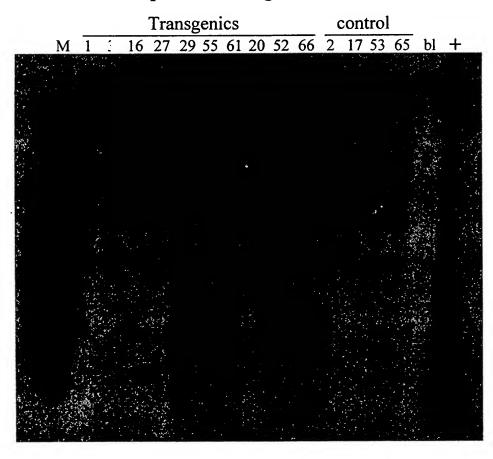


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11/28 Figure 7

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Northern Blot Expression Analysis of TH00-018 Necropsied Transgenic Founders



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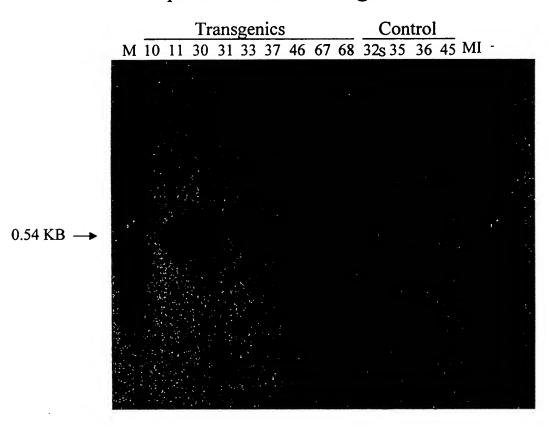


12/28 Figure 8 **RECEIVED**

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Northern Blot Expression Analysis of TH00-018 Hepatectomized Transgenic Founders

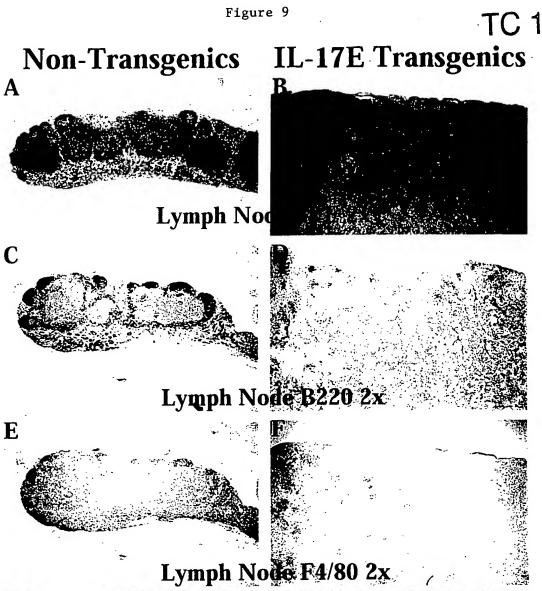






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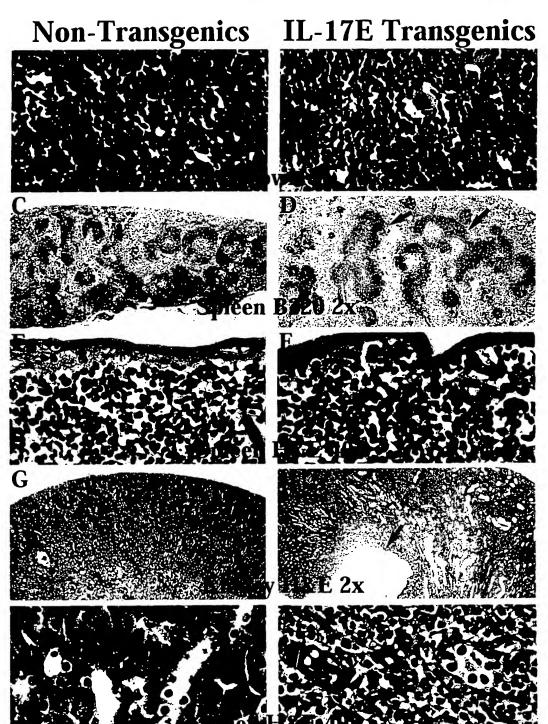
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Figure 10

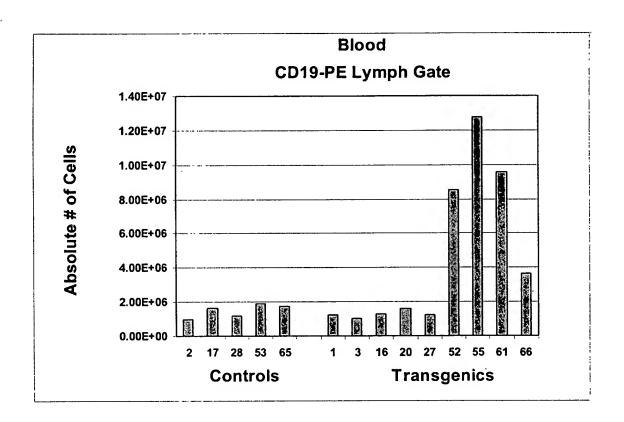


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15/28 Figure 11





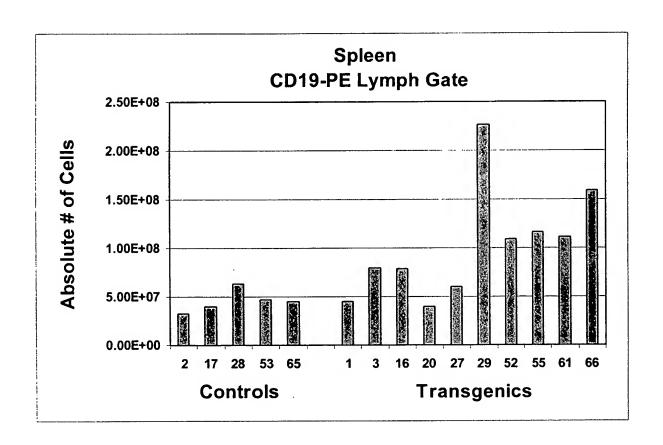


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Figure 12

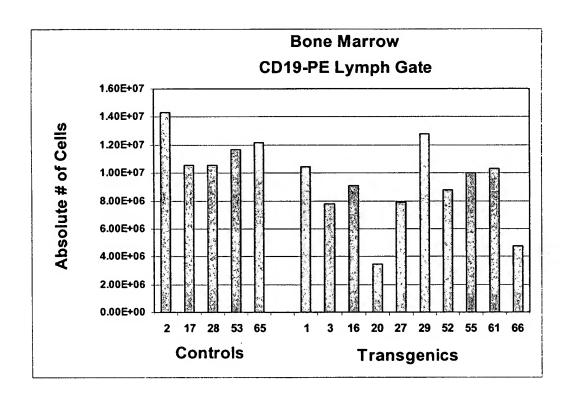






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17/28 Figure 13

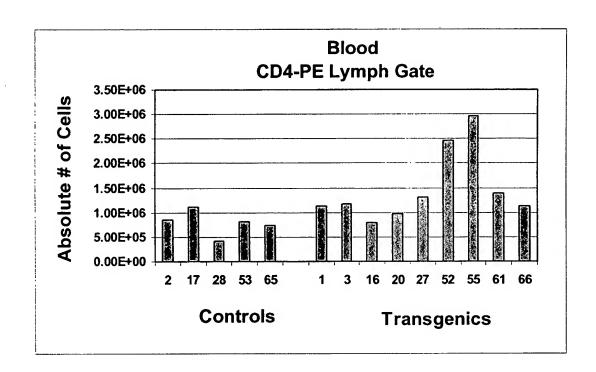






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18/28 Figure 14

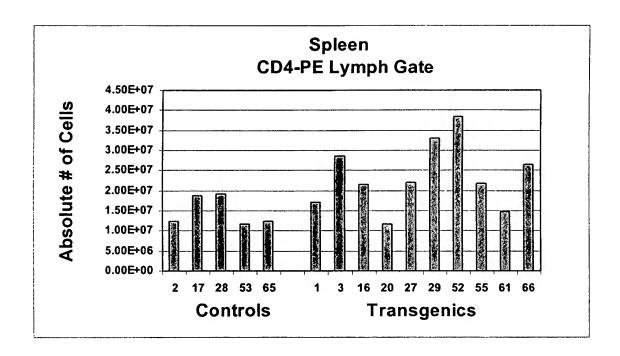






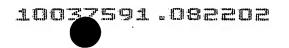
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19/28 Figure 15









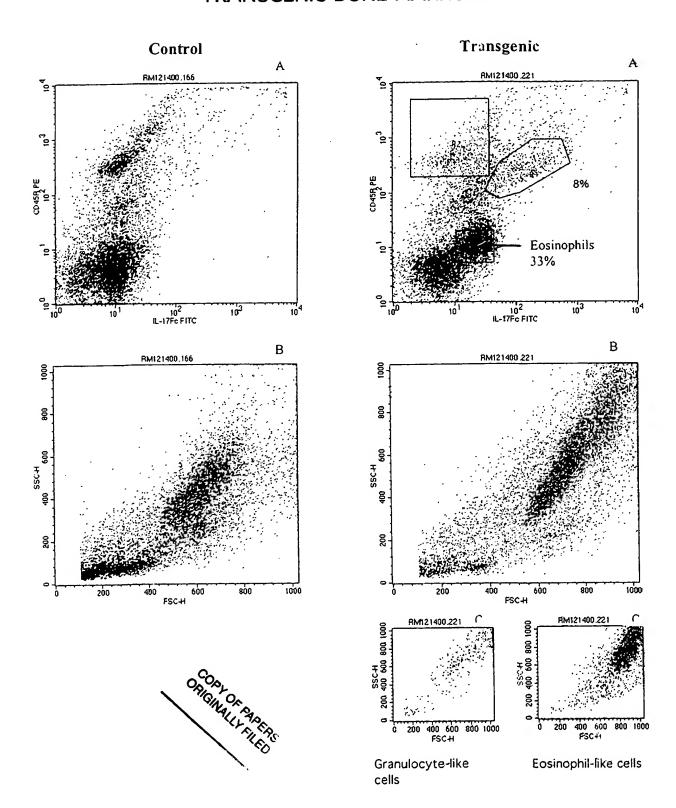
20/28 Figure 16

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CD45R+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE MARROW



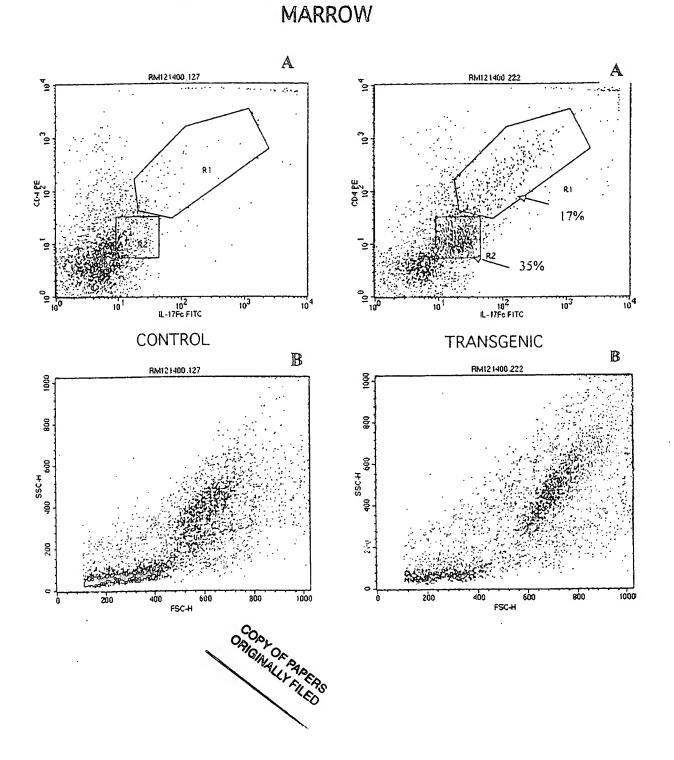


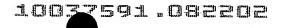
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CD4+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE

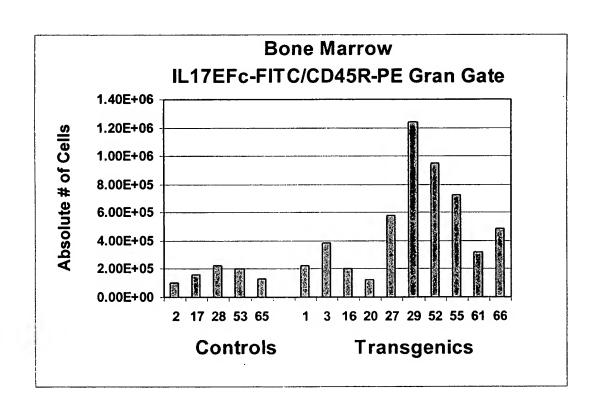






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22/28 Figure 18





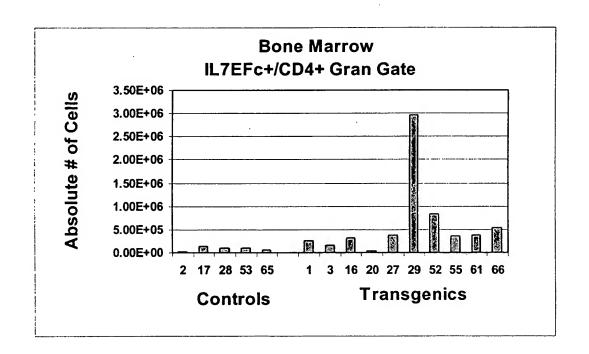


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Figure 19







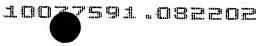
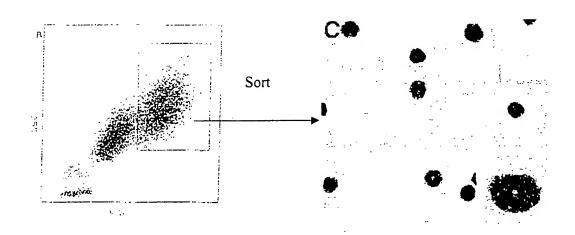
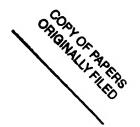


Figure 20

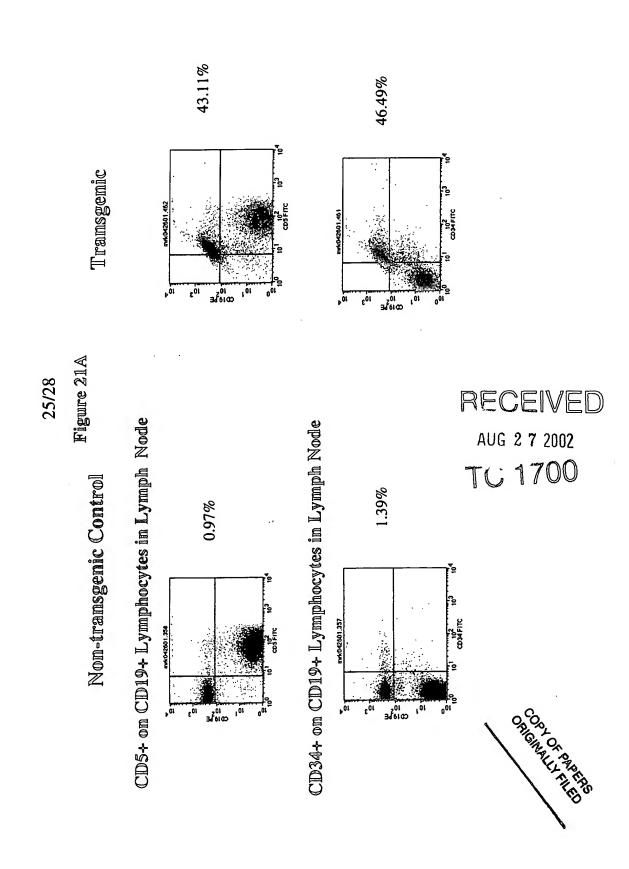


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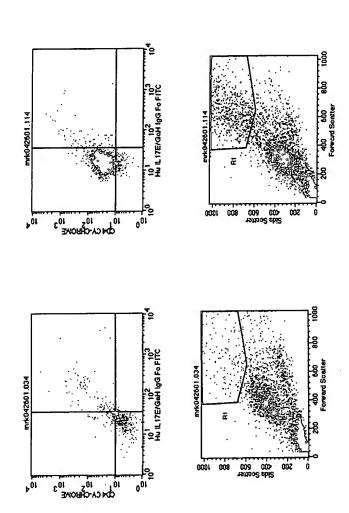






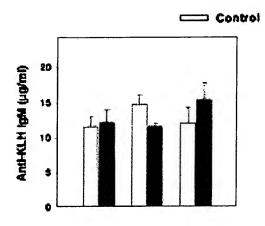
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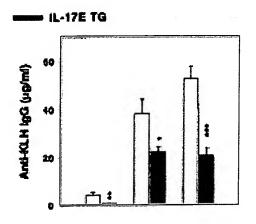
Figure 21B CD4 Expression on Eosimophils in Bone Marrow

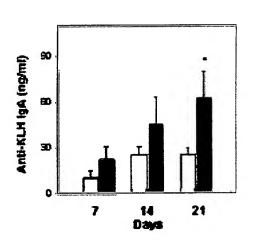


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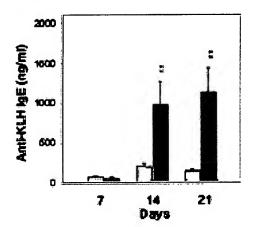
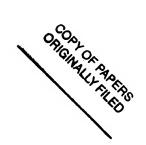


FIG.22



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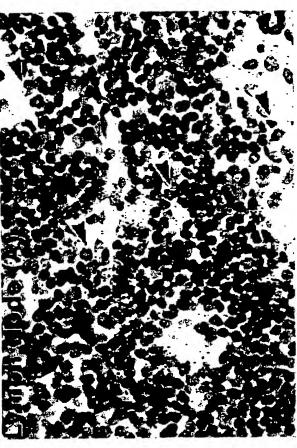




FIG.23